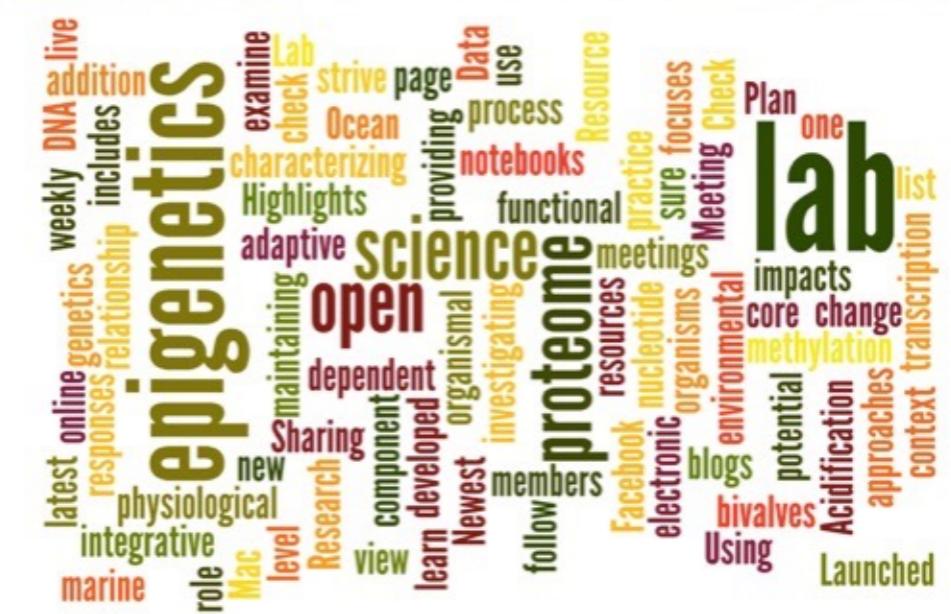


# Towards a functional understanding of DNA methylation in shellfish and implications for aquaculture

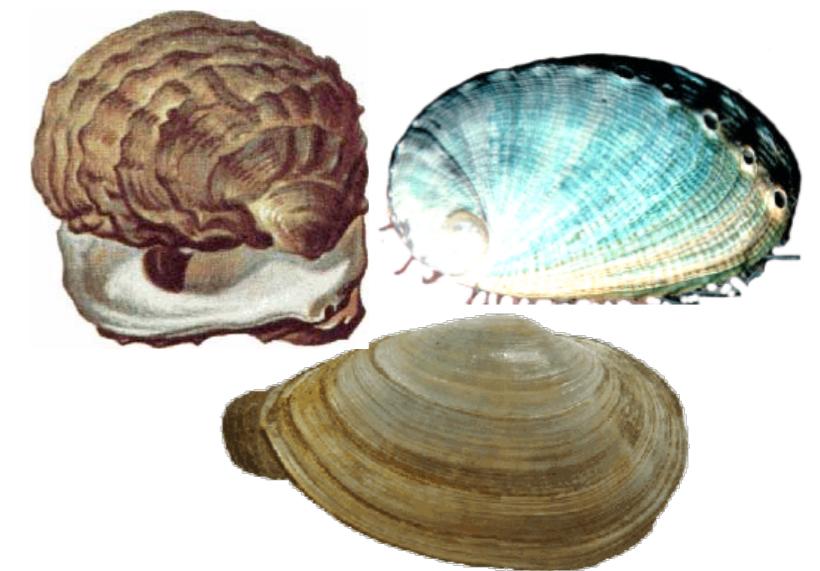
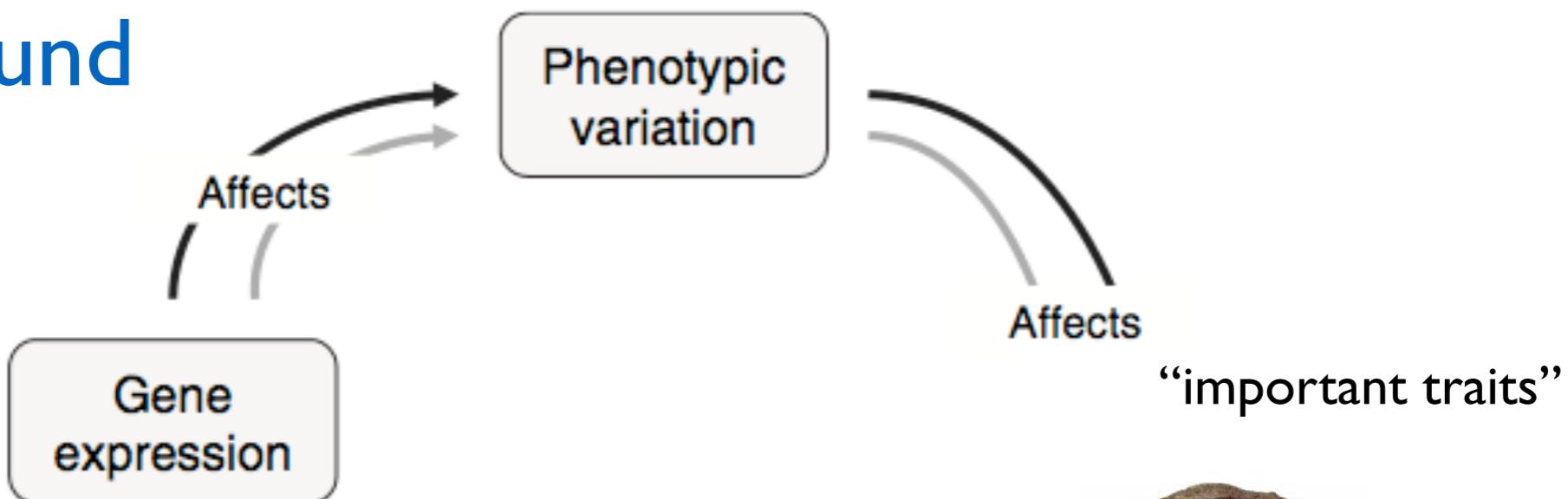
Steven Roberts  
Kenneth K. Chew Endowed Professor  
University of Washington  
School of Aquatic and Fishery Sciences  
**robertslab.info**  
**@sr320**

44<sup>th</sup> Scientific Symposium of the UJNR Aquaculture Panel  
**Genetics and Breeding in Aquaculture**

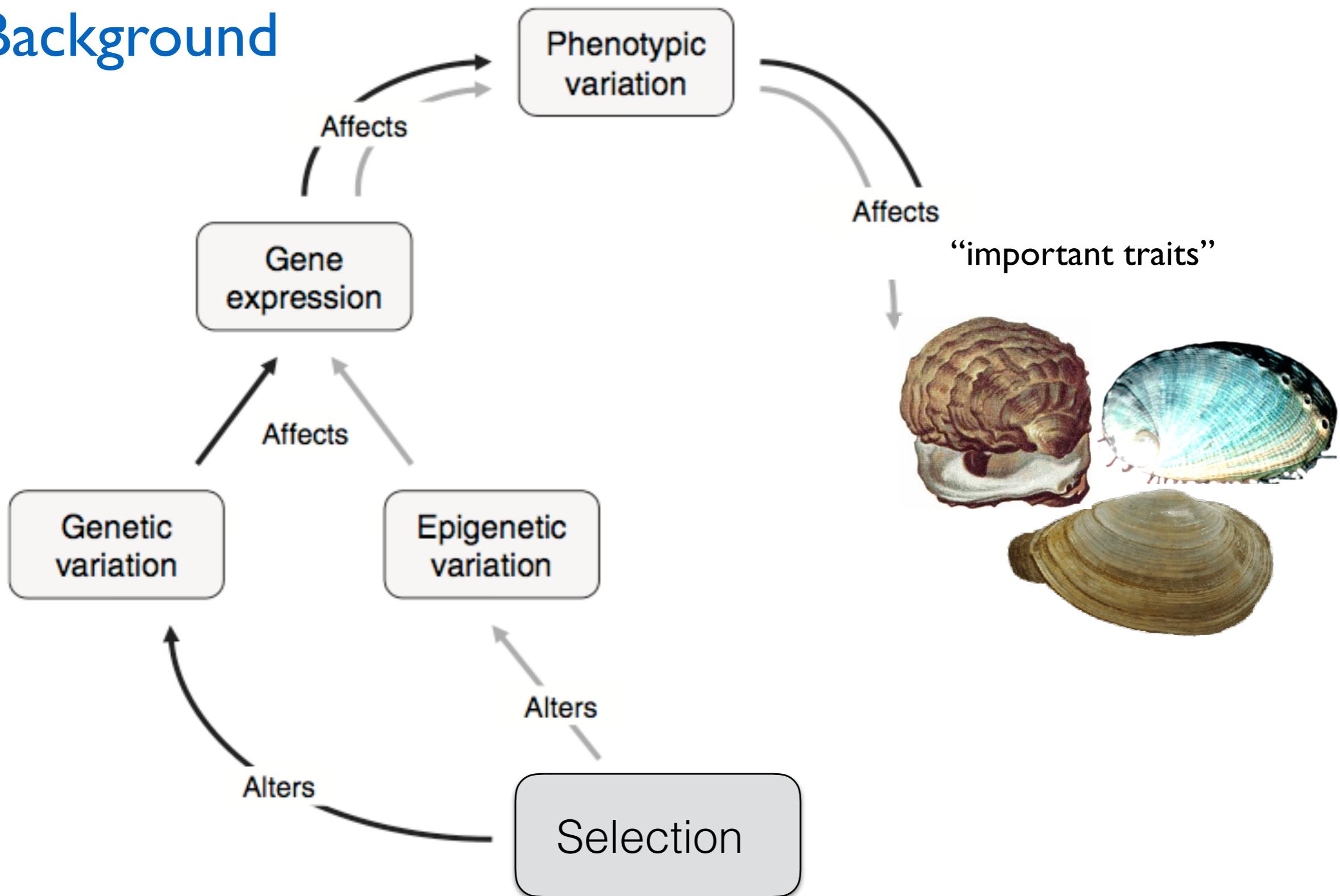
November 2<sup>nd</sup>, 2016



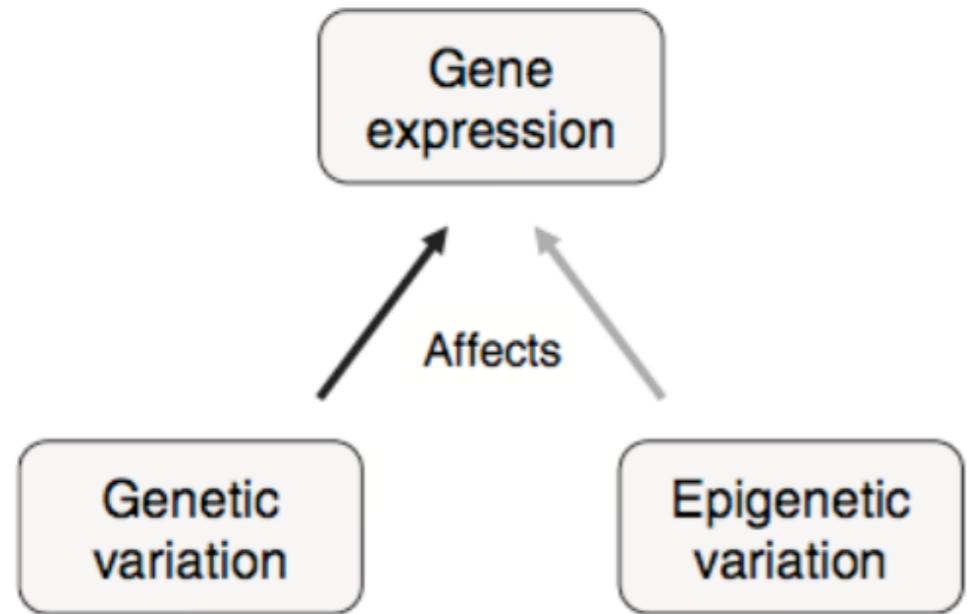
# Background



# Background

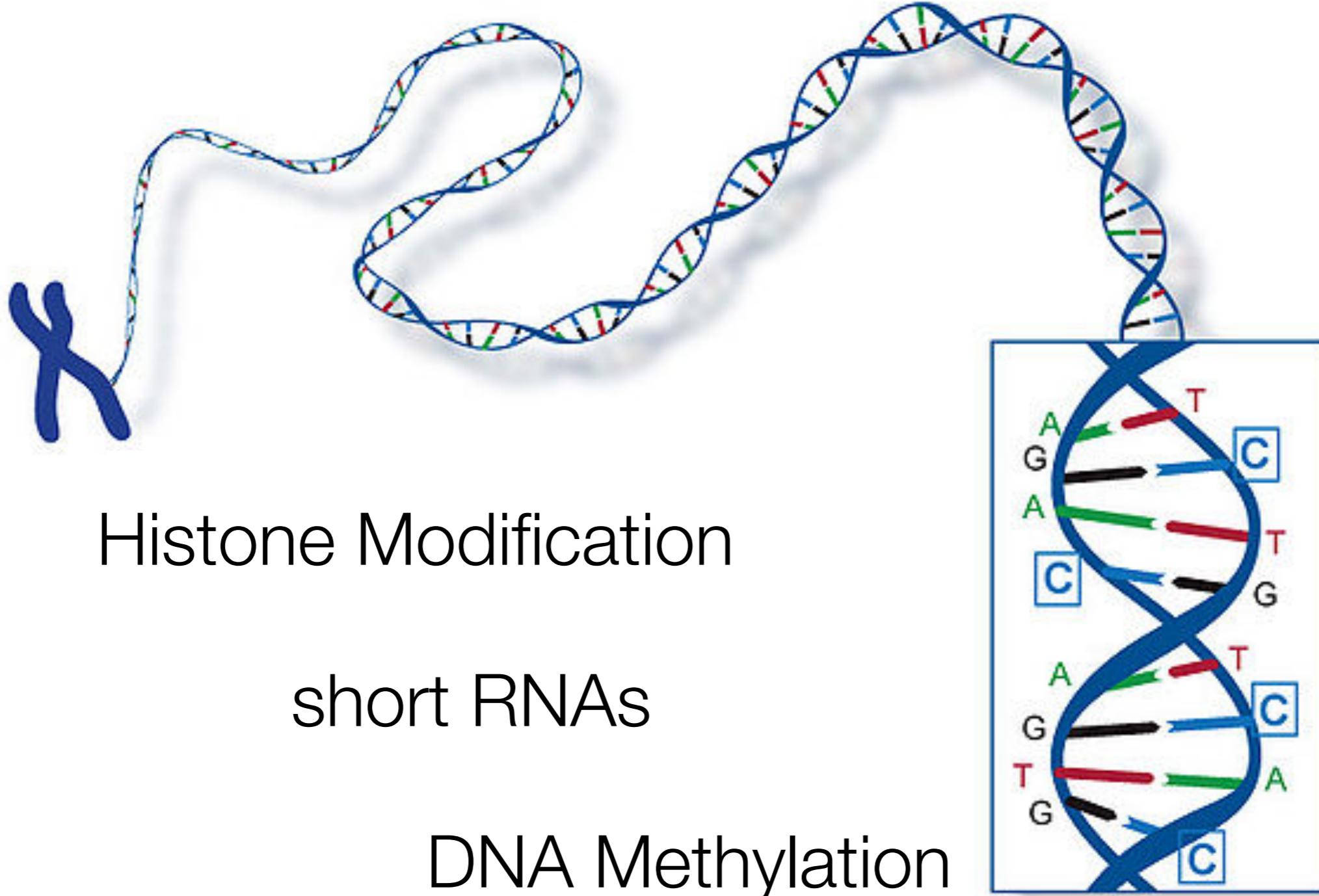


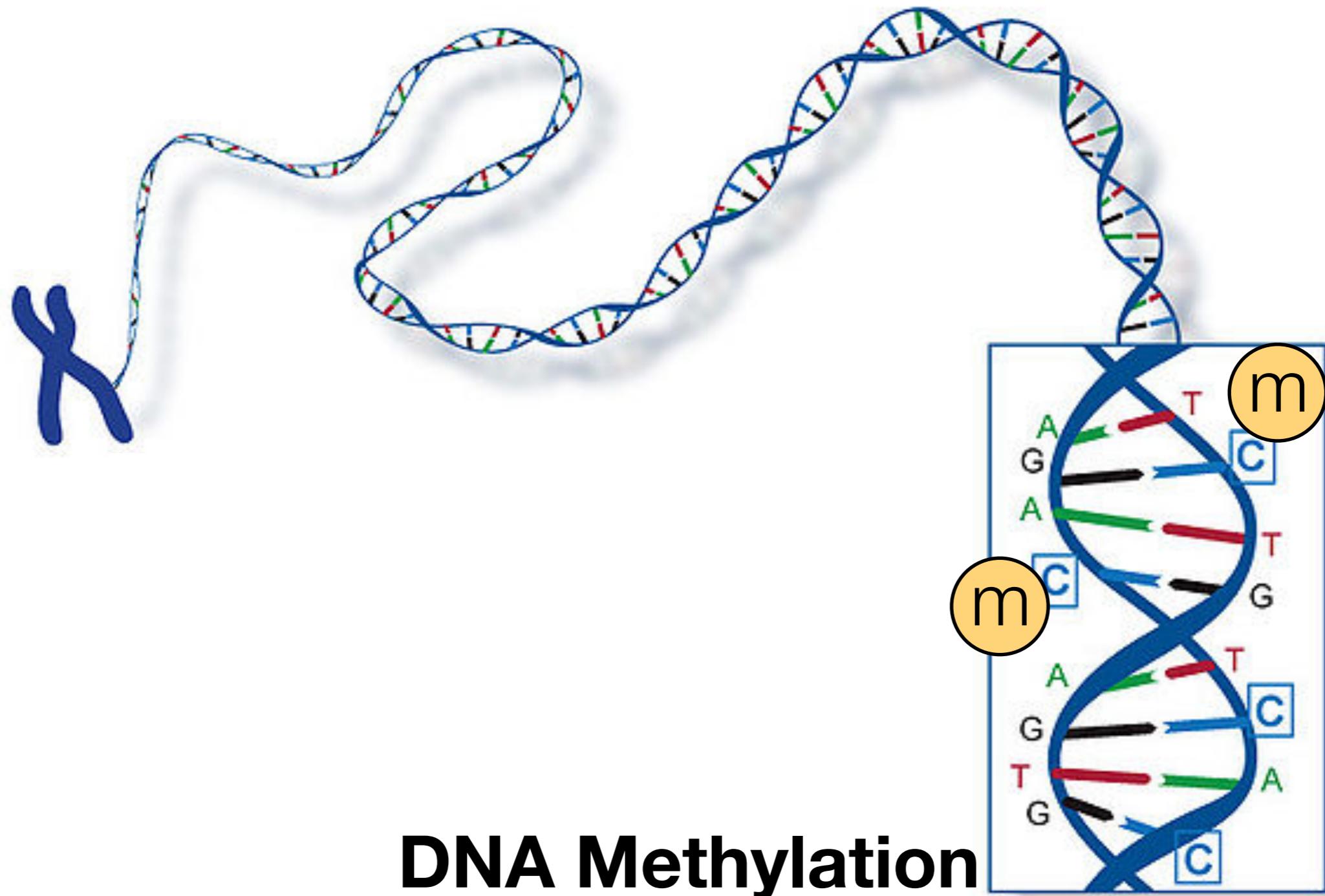
# Big Questions



- 1) To what degree is epigenetic variation heritable?**
- 2) Is epigenetic variation independent of genetic variation?**
- 3) How do environmental conditions influence epigenetic variation?**
- 4) What type of epigenetic phenomenon contributes most to phenotype?**

# Epigenetics





# Outline

**Methylation landscape**

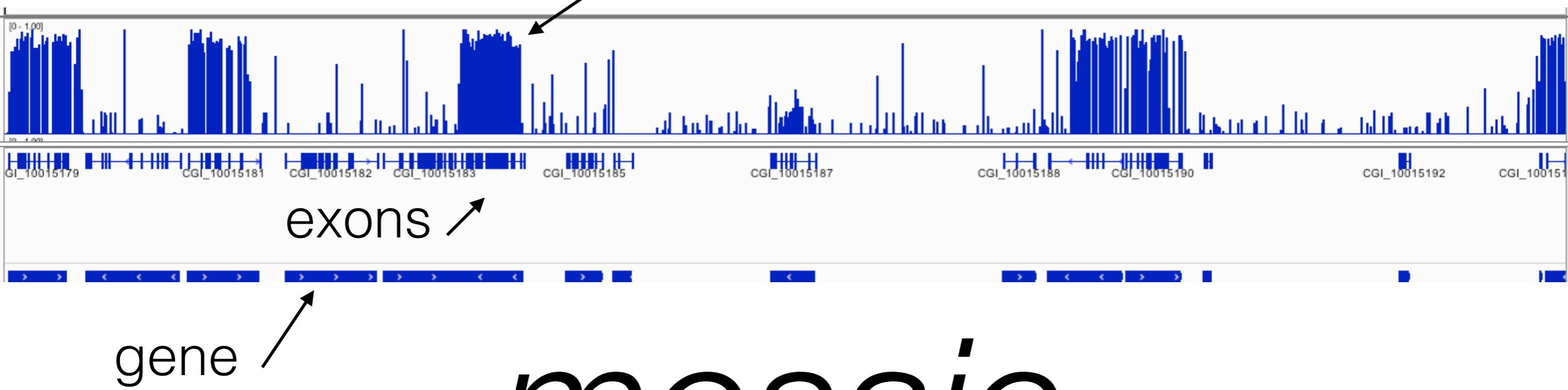
**Population studies**

**Environmental change**

- 1) To what degree is epigenetic variation heritable?
- 2) Is epigenetic variation independent of genetic variation?
- 3) How do environmental conditions influence epigenetic variation?

# Methylation landscape

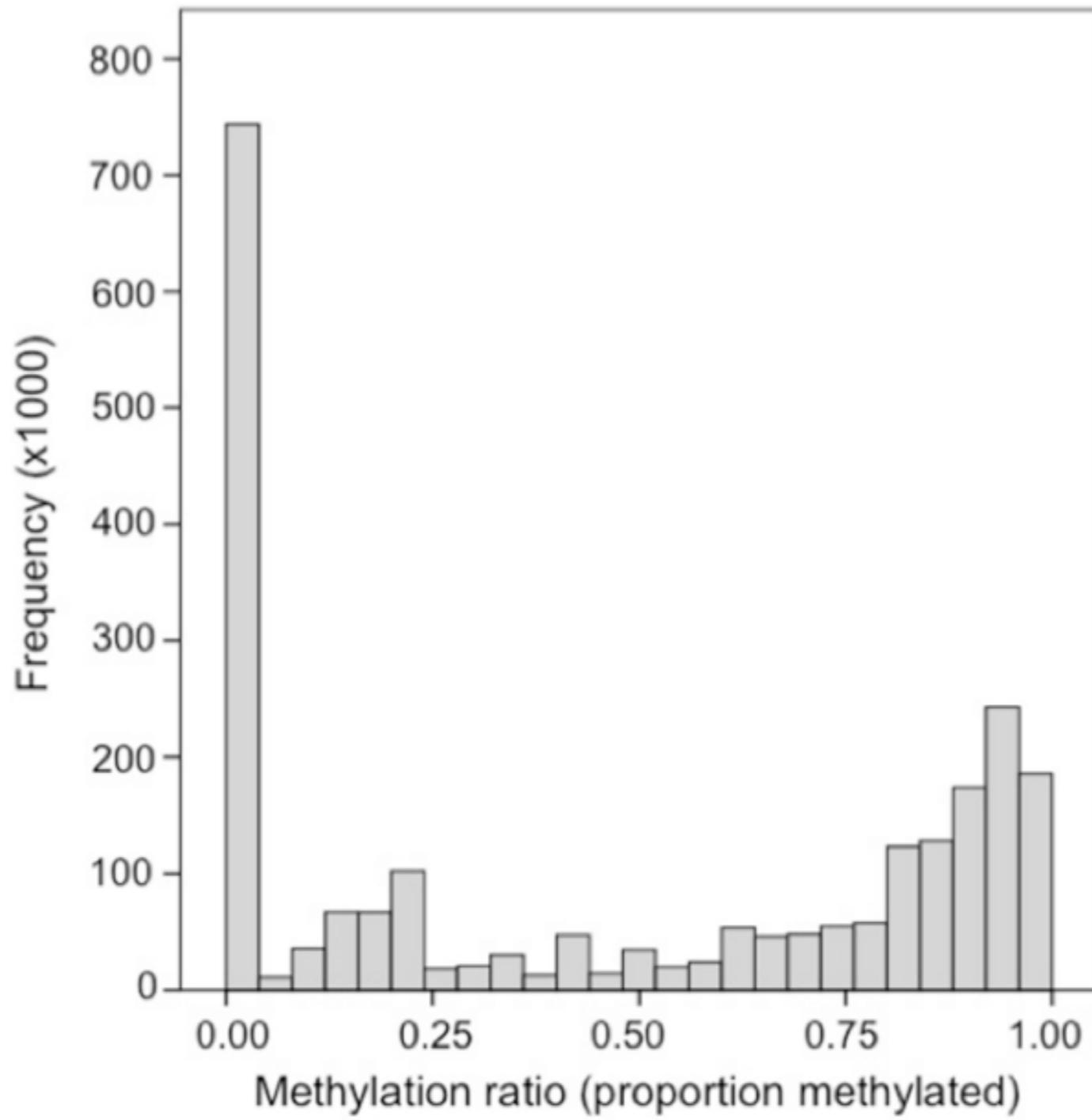
DNA methylation level (0-100%) @ cytosines



*mosaic*

associated with gene bodies

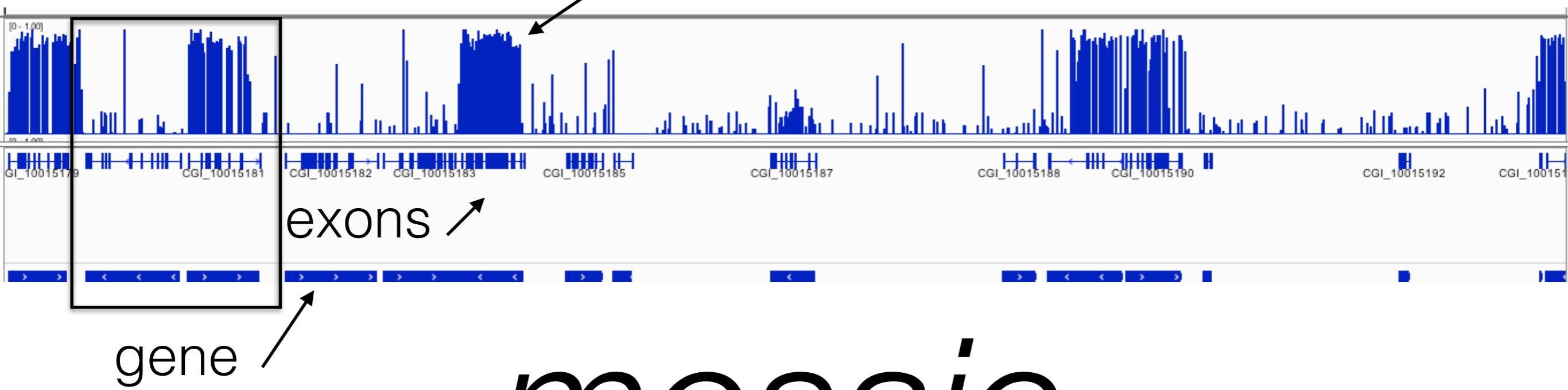
# Methylation landscape



**Figure 1** Frequency distribution of methylation ratios for CpG dinucleotides in oyster gill tissue. A total of 2,625,745 CpG dinucleotides with  $\geq 5 \times$  coverage are represented.

# Methylation landscape

DNA methylation level (0-100%) @ cytosines

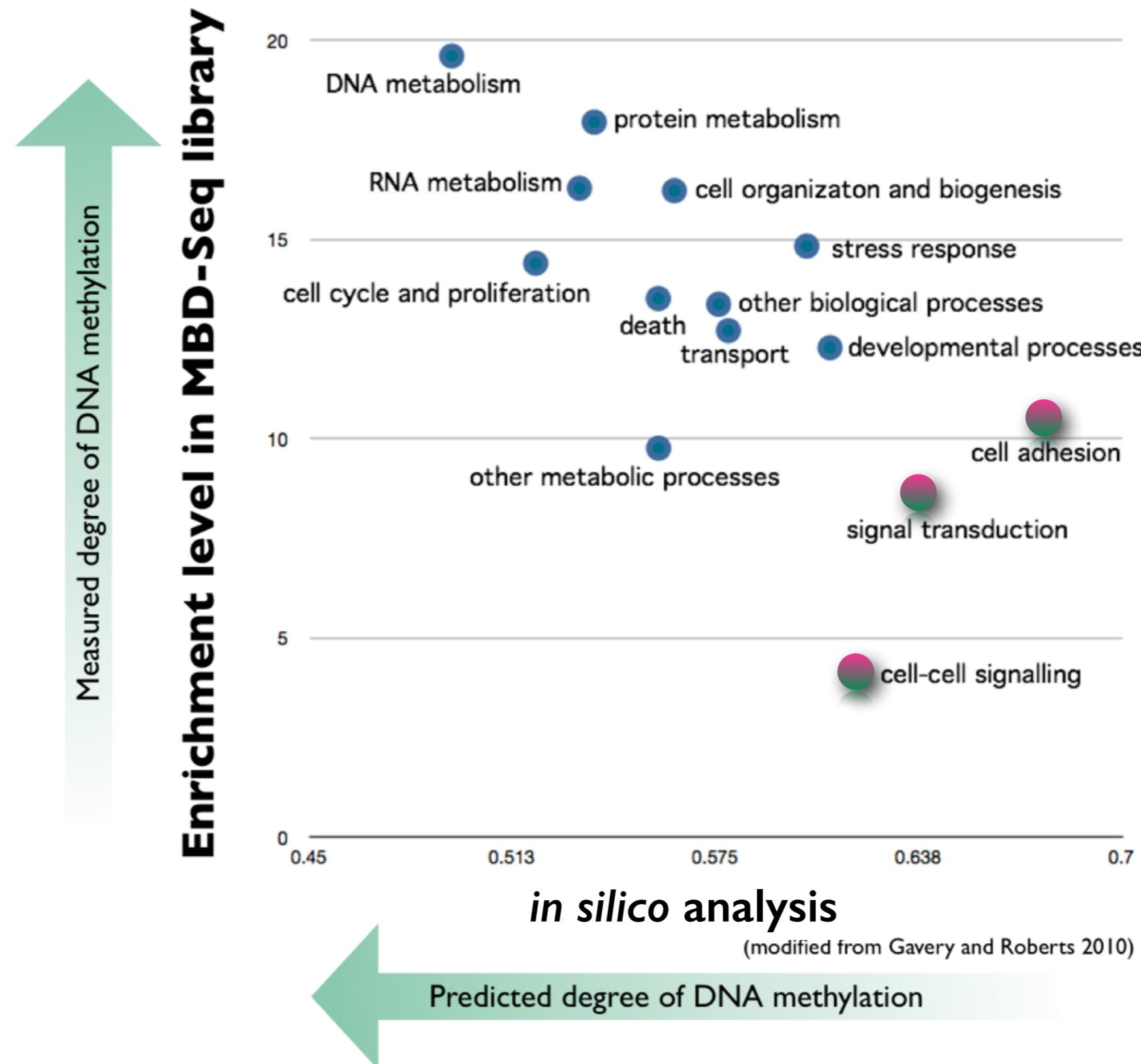


# *mosaic*

Why are only a subset of genes methylated?

associated with gene bodies

# Methylation landscape



# Outline

1) To what degree is epigenetic variation heritable?

Methylation landscape

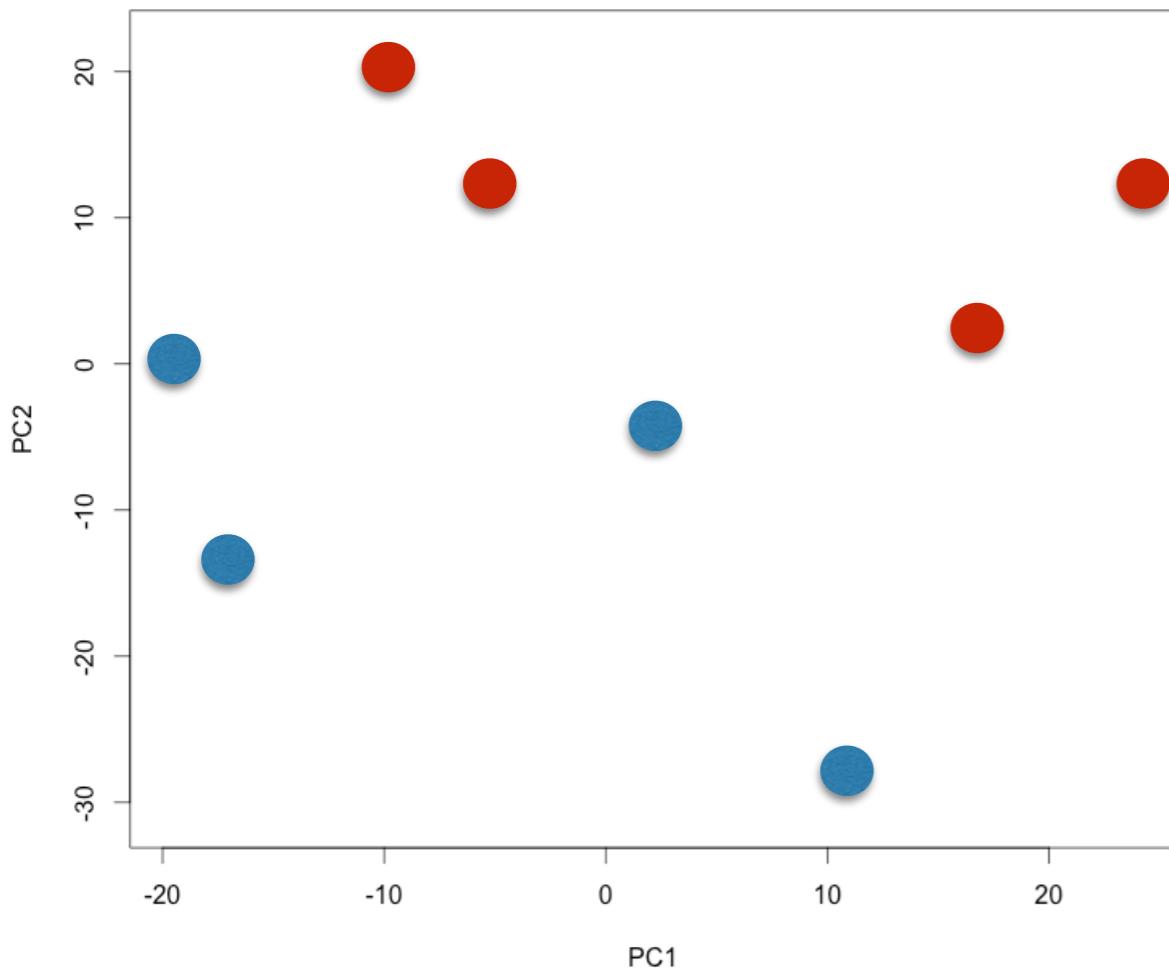
2) Is epigenetic variation independent of genetic variation?

Population studies

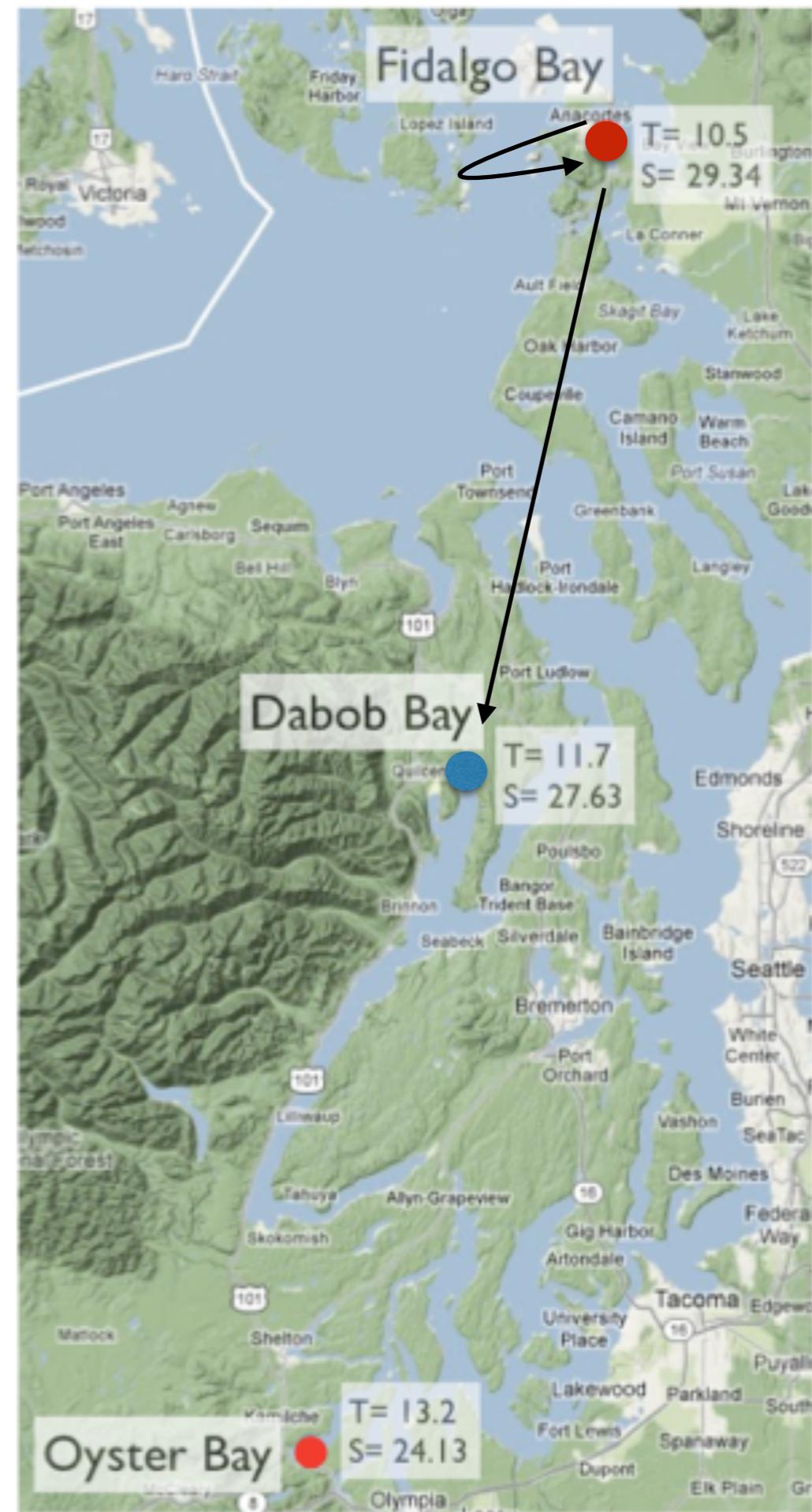
3) How do environmental conditions influence epigenetic variation?

Environmental change

CpG methylation PCA Analysis



DNA methylation  
siblings grown different sites





## Reciprocal Transplant Experiment



Manchester

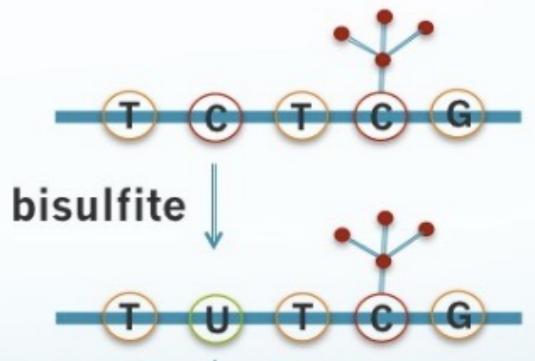


## Reciprocal Transplant Experiment



Epigenetic variation **1**

# Family and Developmental Variation



Sperm &  
Larvae  
(72h & 120h)



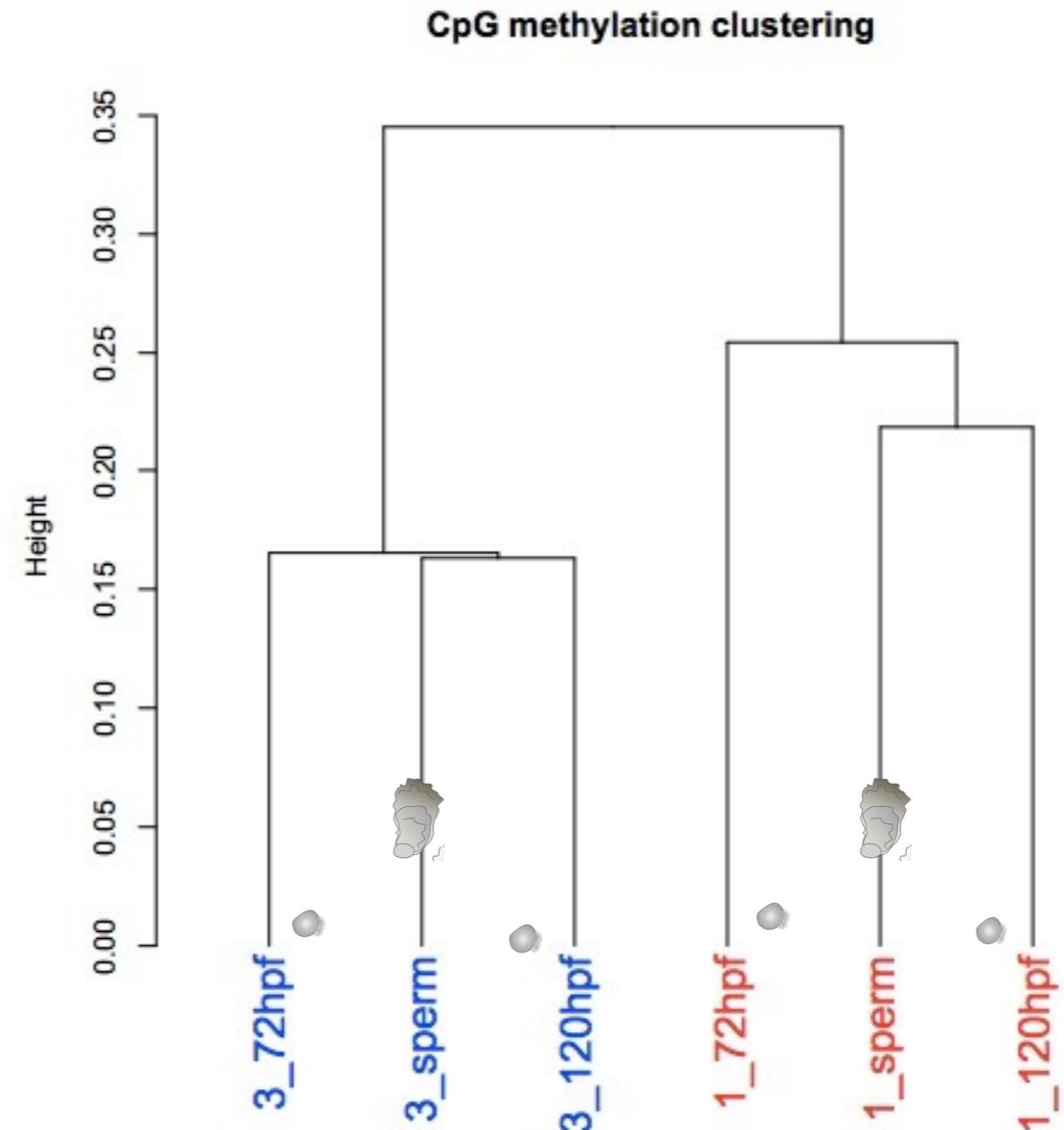
**bioRxiv**  
beta  
THE PREPRINT SERVER FOR BIOLOGY

New Results

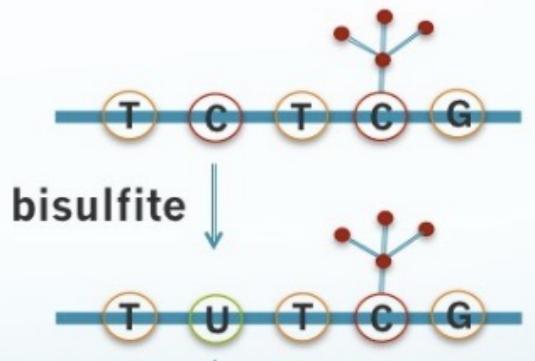
**Indication of family-specific DNA methylation patterns in developing oysters**

Claire E. Olson , Steven B. Roberts

doi: <http://dx.doi.org/10.1101/012831>



# Family and Developmental Variation



## Inheritance



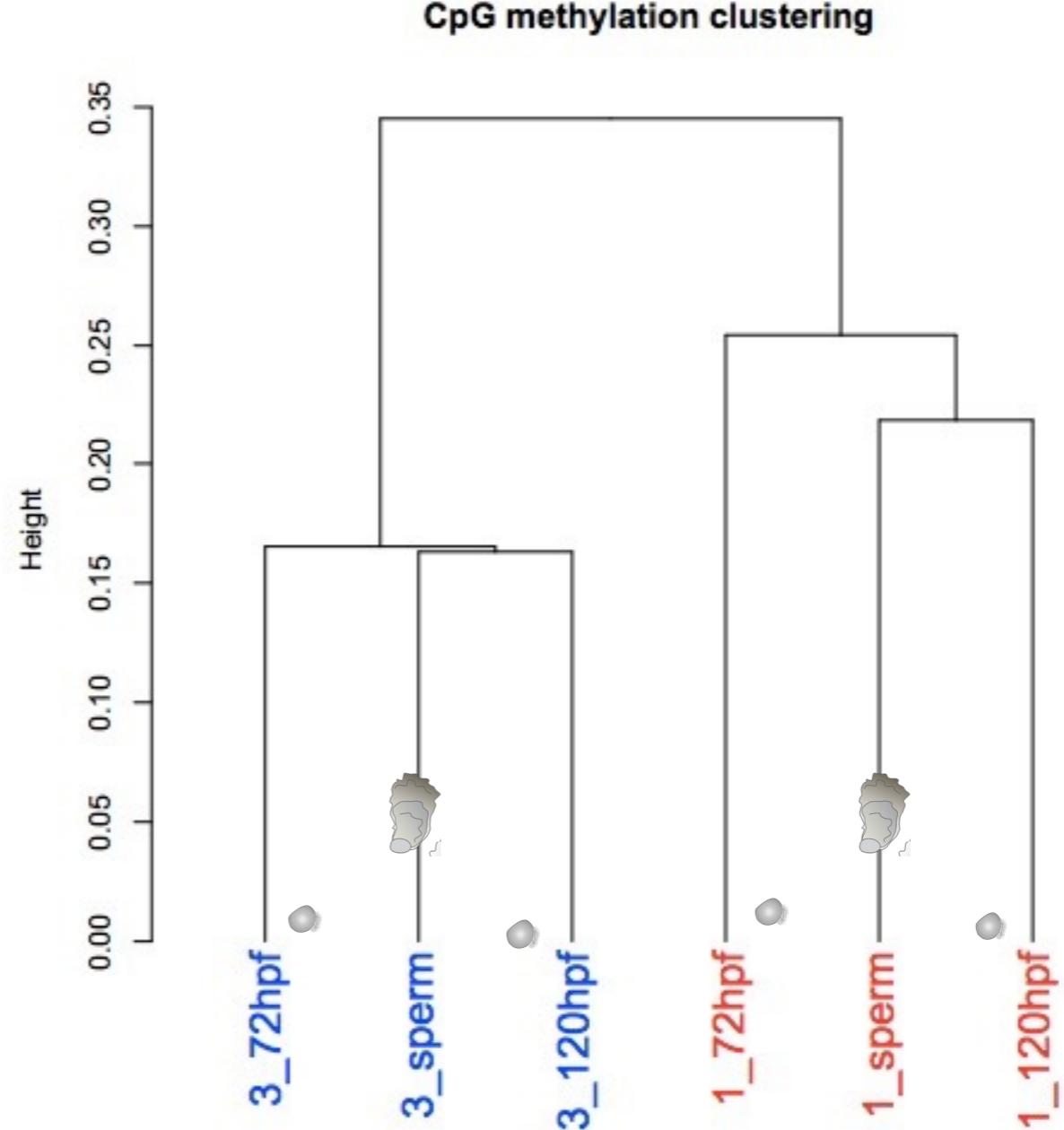
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New Results

**Indication of family-specific DNA methylation patterns in developing oysters**

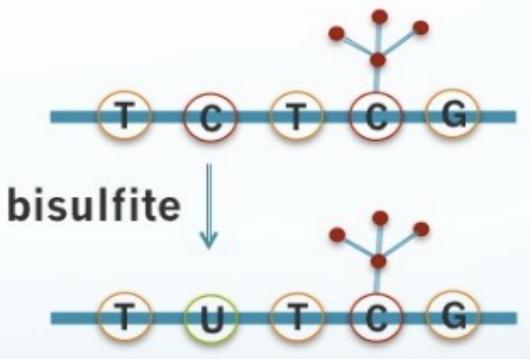
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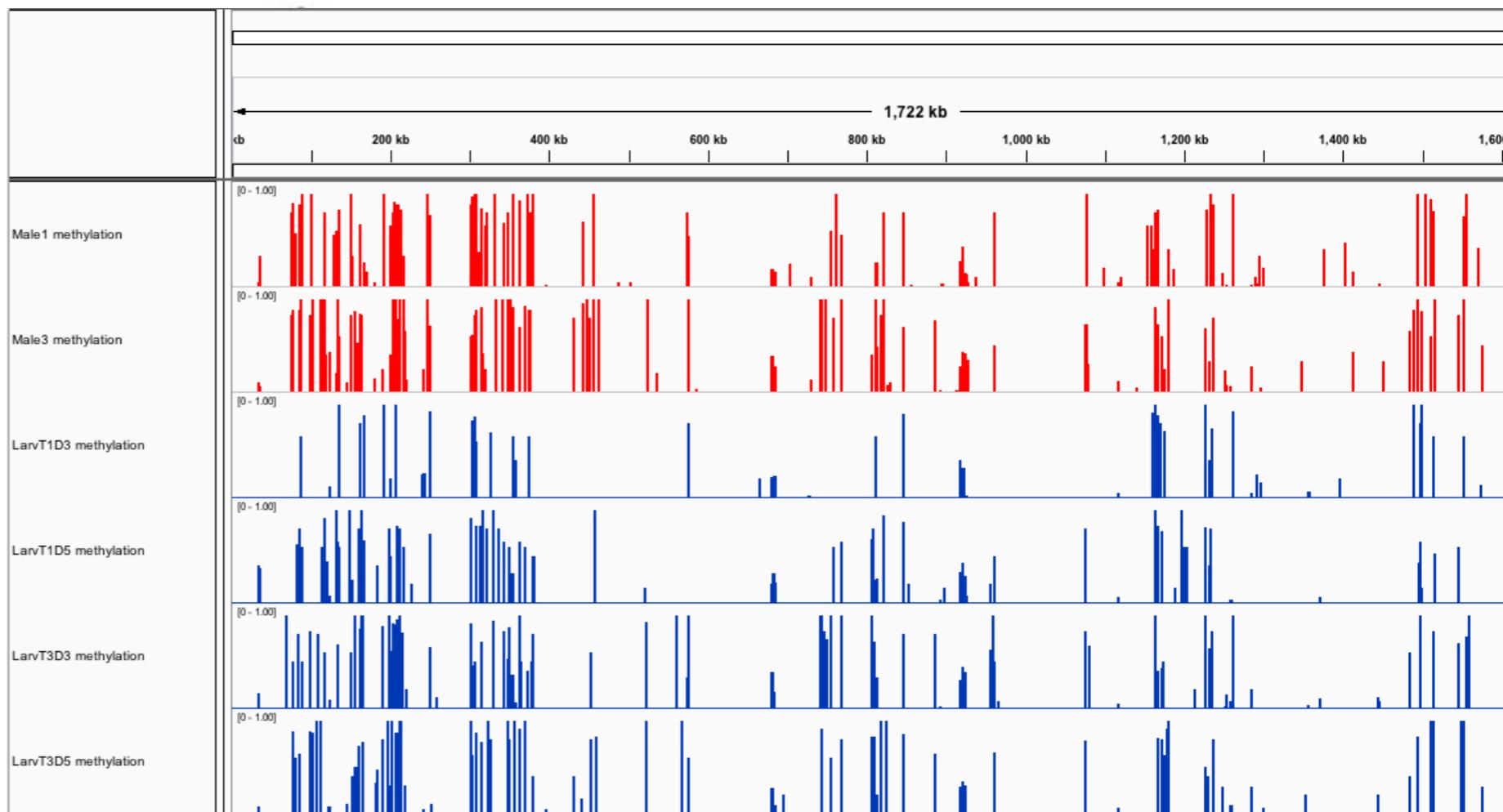


## Epigenetic variation 1

# *Family and Developmental Variation*



# Sperm & Larvae (72h & 120h)



DNA methylation level (0-100%) @ cytosines



bioRxiv

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New Results

## Indication of family-specific DNA methylation patterns in developing oysters

Claire E. Olson , Steven B. Roberts

**doi:** <http://dx.doi.org/10.1101/012831>

# Outline

1) To what degree is epigenetic variation heritable?

Methylation landscape

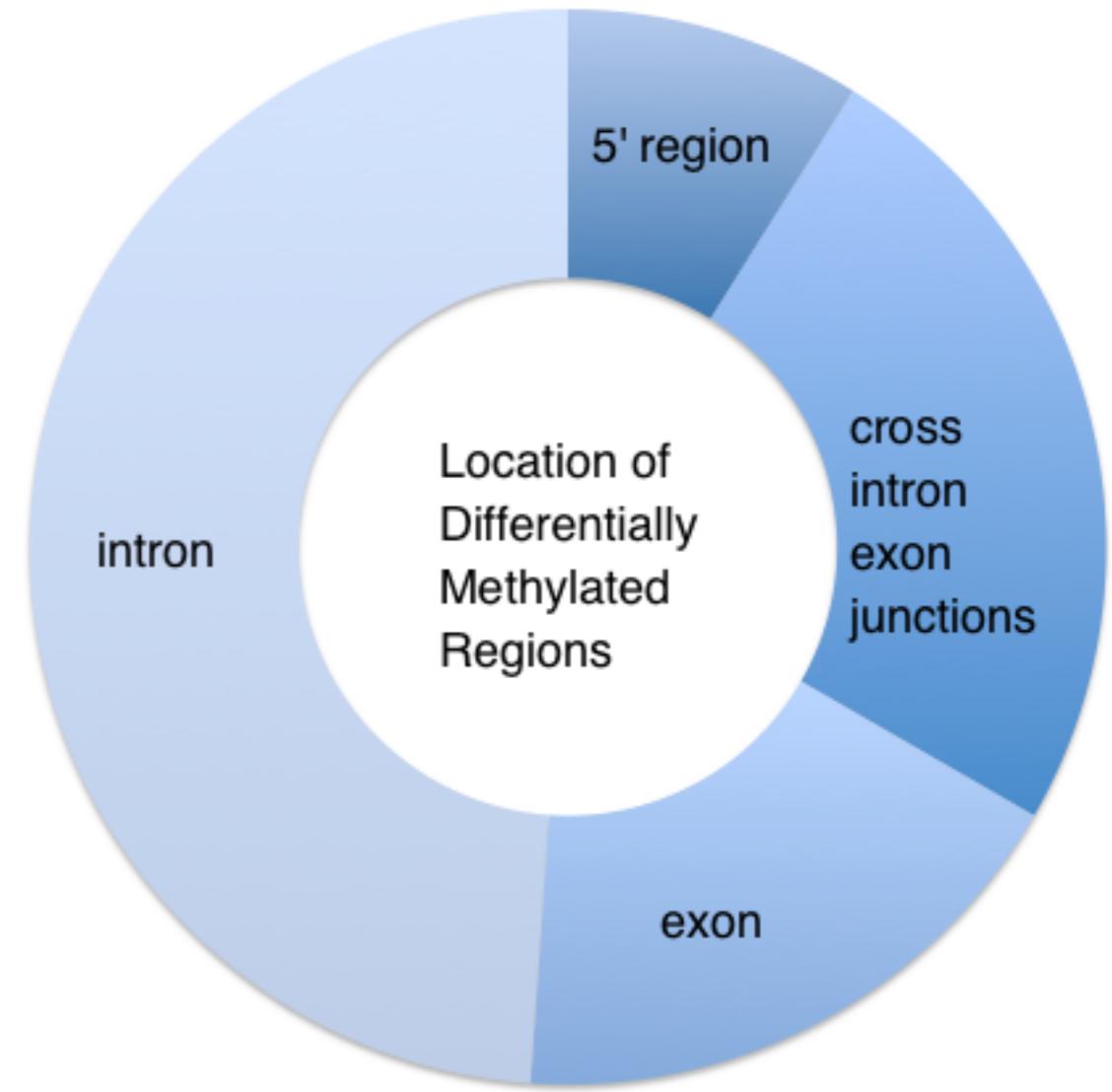
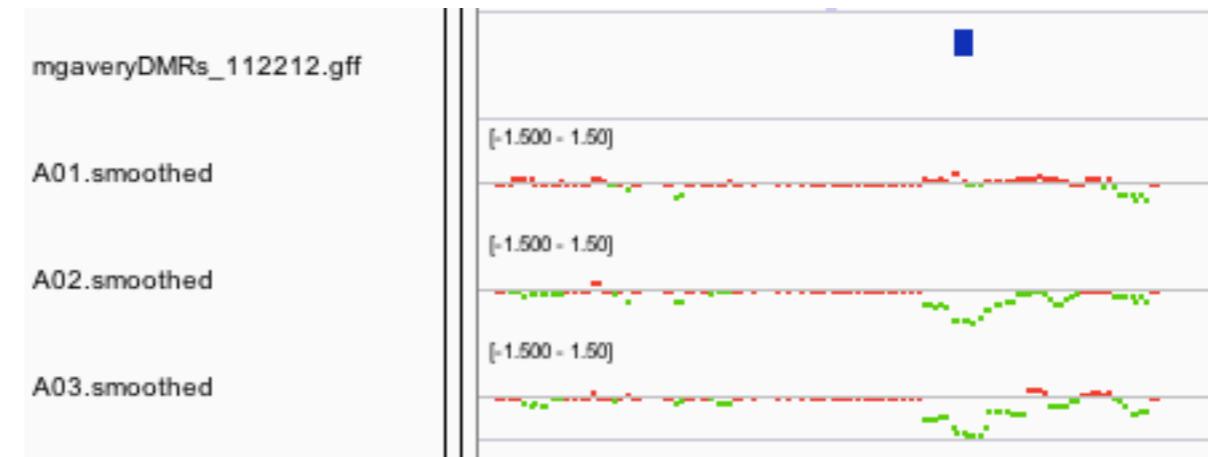
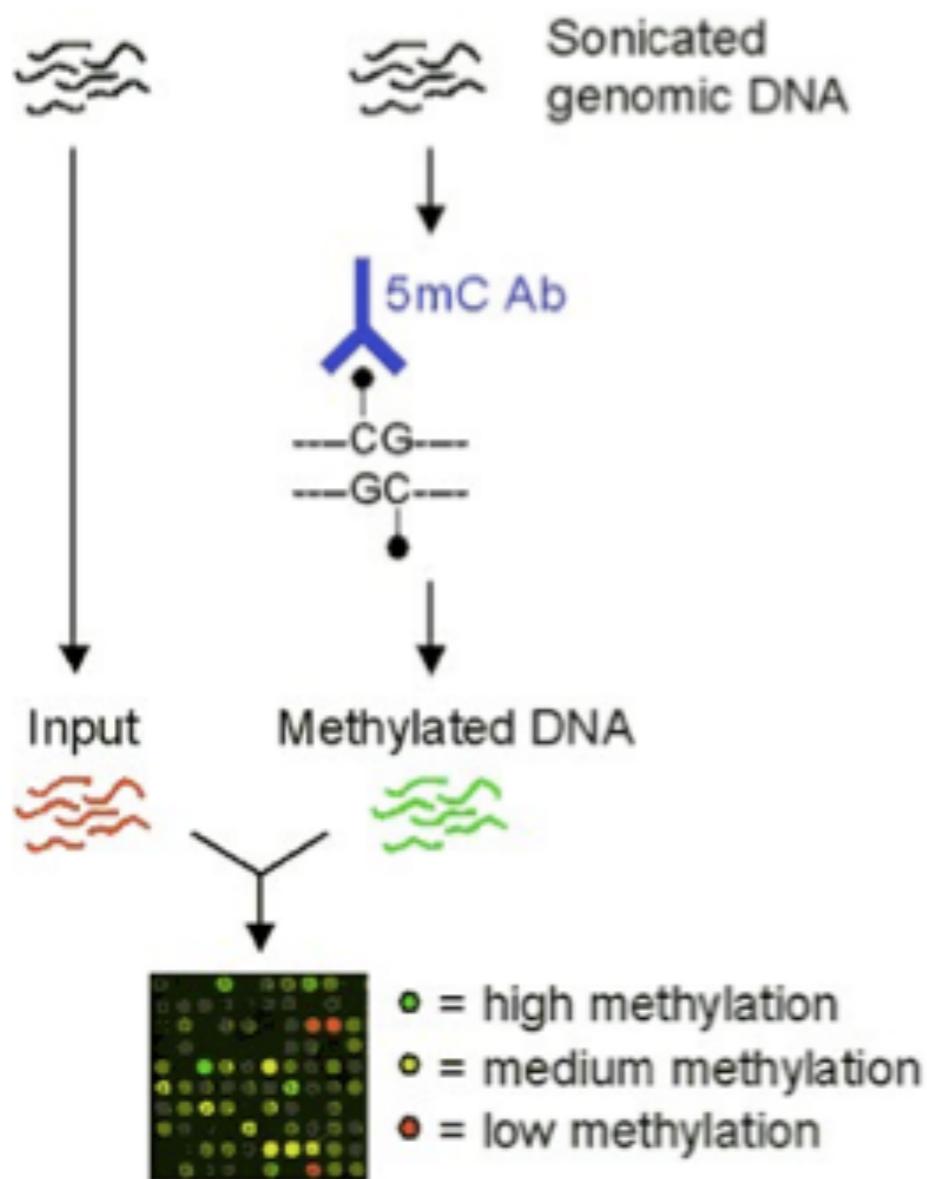
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Population studies

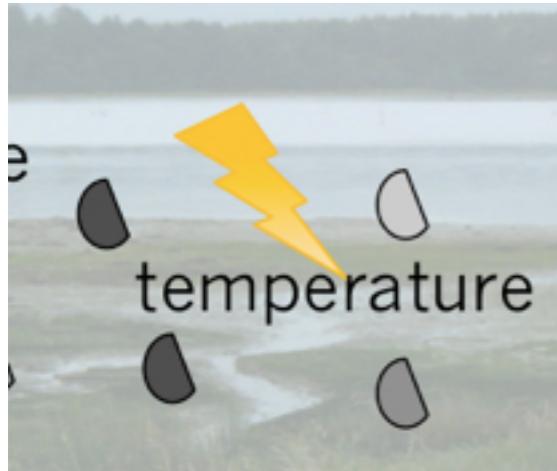
3) How do environmental conditions influence epigenetic variation?

Environmental change

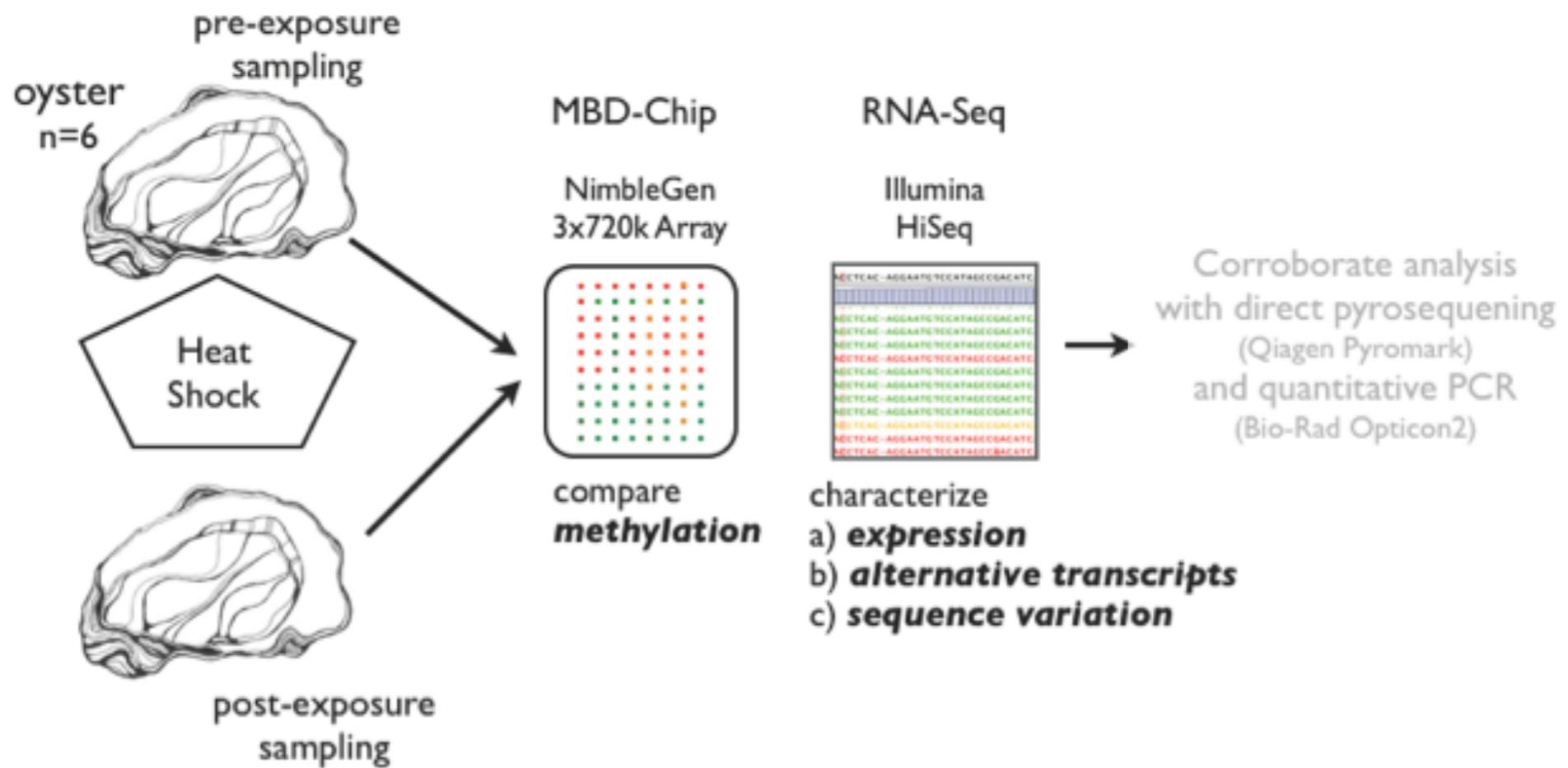
# Environmental impact (Estrogens)



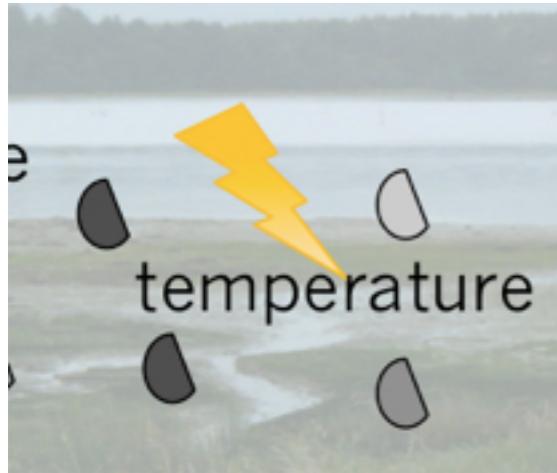
# Environment and gene expression



*stochastic or targeted?*



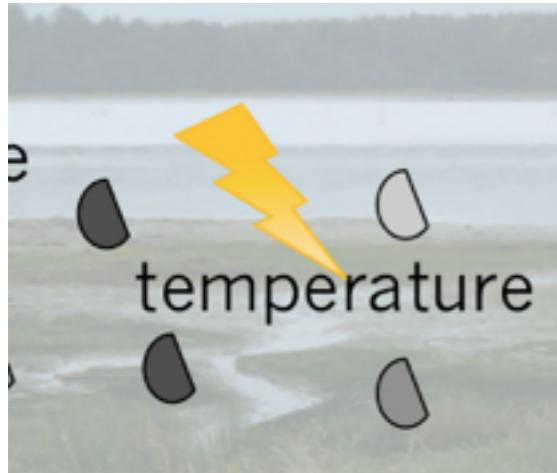
# Environment and gene expression



*stochastic or targeted?*

Oyster	Hypo-methylated	Hyper-methylated
2	7224	2803
4	6560	3587
6	7645	4044

# Environment and gene expression

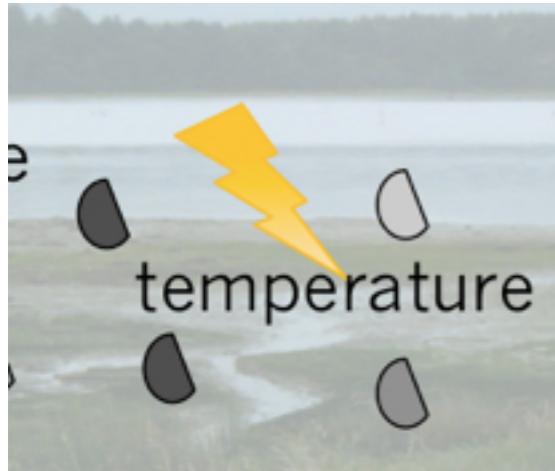


*stochastic or targeted?*

Oyster	Hypo-methylated	Hyper-methylated
2	7224	2803
4	6560	3587
6	7645	4044

No obvious association  
with genome feature  
including *differentially*  
*expressed*  
*genes*

# Environment and gene expression



*stochastic or targeted  
or ..?*

Oyster	Hypo-methylated	Hyper-methylated
2	7224	2803
4	6560	3587
6	7645	4044

Changes in methylation (either direction) are more prevalent in introns, repeats, and transposable elements.

# Take Home

*Oyster genome has a fantastic degree of diversity contributing to phenotypic plasticity & adaptation potential.*

# Take Home

*Oyster genome has a fantastic degree of diversity contributing to phenotypic plasticity & adaptation potential.*

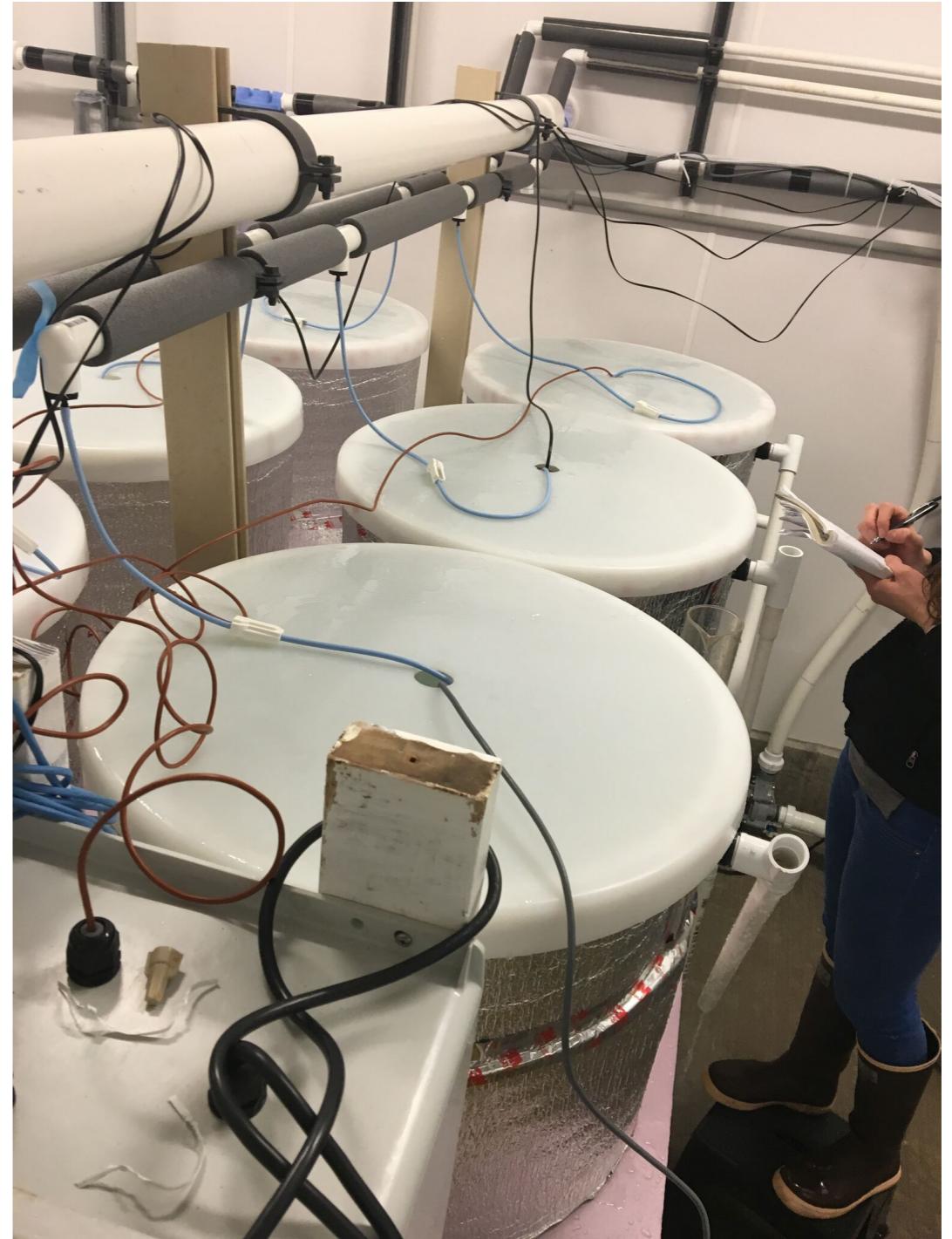
- large gene families
- very high mutation rate (snp/50bp)
- numerous exons per gene (potential for alternatives)
- genome full of repeats region
- high number of transposable elements
- lack of methylation of transposable suggest mobility
- family variation of methylation
- limited methylation environmental response genes  
is associated with spurious transcription
- inheritance of epigenetic marks as mechanism of improved adaptation

# Very new ~~data~~

## Selection

## Ocean Acidification

*Panopea generosa*



# Very new data

## Selection Ocean Acidification

Day 10

Control: Random Mortality

~42% ACGCTGATCGT

~38% ACGCTAATCGT

Day 1

Proportion of sequences in pooled  
larvae sample with given allele (G vs A)

~42% ACGCTGATCGT

~38% ACGCTAATCGT

Day 10

High  $p\text{CO}_2$ : Non-random  
Mortality

~80% ACGCTGATCGT

~20% ACGCTAATCGT

Day 1

Evidence of allele beneficial (G) to survival  
under High  $p\text{CO}_2$  conditions

High  $p\text{CO}_2$   
Ambient temperature

High  $p\text{CO}_2$   
High temperature

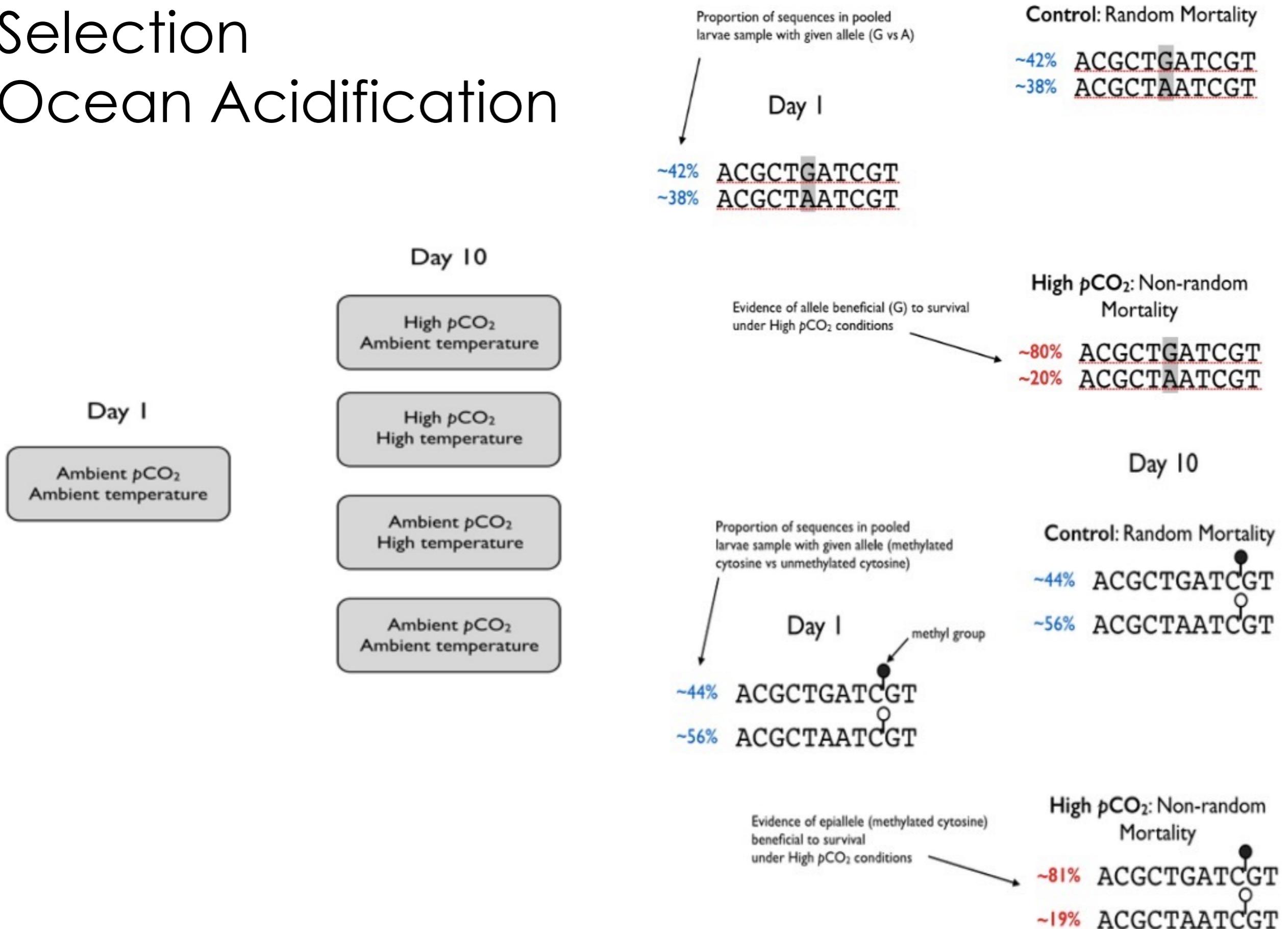
Ambient  $p\text{CO}_2$   
High temperature

Ambient  $p\text{CO}_2$   
Ambient temperature

Ambient  $p\text{CO}_2$   
Ambient temperature

# Very new data

## Selection Ocean Acidification



# Acknowledgements

Mackenzie Gavery

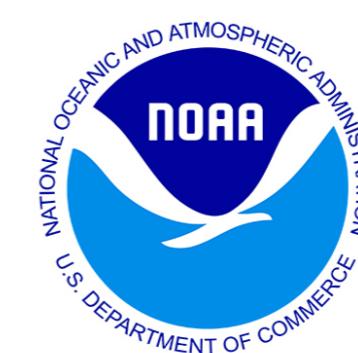
Claire Olson

Sam White

Brent Vadopalas

Hollie Putnam

Laura Spencer



slides, data & more @

[github.com/sr320/talk-univ-perp-2016](https://github.com/sr320/talk-univ-perp-2016)